```
axmi007   -----MNQNNNNEYEIIDSKNLSYPSNRNIDHSRYPYTNNPNQPLQNTNYKEWLNMCQGN  55
cry1Aa    -------------------MDNNPNINECIPYN---CLSNPE--------------VEVL  24
cry1Ac    -------------------MDNNPNINECIPYN---CLSNPE--------------VEVL  24
cry1Ia    --------MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQNINHEDCLKMSEYE  49
cry3Aa1   MIRKGGRKMNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADN  60
cry3Ba    MIRMGGRKMNPNNRSEYDTIKVTPNSELPTNHNQYPLADNPNSTLEELNYKEFLRMTADN  60
cry4Aa    ----MNPYQNKNEYETLNASQKKLNISN--NYTRYPIENSPKQLLQSTNYKDWLNMCQQN  54
cry6Aa    ----------------------------------------------------------
cry7Aa    -------MNLNNLD--GYEDSNRTLNNSLNYP---TQKALSPSLKNMNYQDFLSITERE  47
cry8Aa    -------MSPNNQNEYEIIDATPSTSVSSDSNRYPFANEPTDALQNMNYKDYLKMSGGE  52
cry10Aa   ----MNPYQNKNEYEIFNAPSNGFSKSN--NYSRYPLANKPNQPLKNTNYKDWLNVCQDN  54
cry16Aa   ----MHYYGNRNEYDILNASSNDSNMSN--TYPRYPLANPQQDLMQNTNYKDWLNVCEGY  54
cry19Ba   ----MNSYQNKNEYEILDAKRNTCHMSN--CYPKYPLANDPQMYLRNTHYKDWINMCEEA  54
cry24Aa   ----MNQYQNKNEYEILESSQNNMNMPN-----RYPFADDPNAVMKNGNYKDWVNECEGS  51


axmi007   TQYGDNFETFASADTIAAVSAGTIVSGTLLAGIGGLTSISGPIGIIGAIIISFGTLITVF  115
cry1Aa    G-------GERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLG-------LVDIIWGIF  68
cry1Ac    G-------GERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLG-------LVDIIWGIF  68
cry1Ia    N-------VEPFVS-ASTIQTGIGIAGKILGTLGVPFAGQVAS-------LYSFILGEL  93
cry3Aa1   N-----TEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVS-------FYTNFLNTI  107
cry3Ba    S-----TEVLDSSTVKDAVGTGISVVGQILGVVGVPFAGALTS-------FYQSFLNAI  107
cry4Aa    QQYGGDFETFIDSG---ELSAYTIVVGTVLTGFGFTTPLG-------LALIGFGTLIPVL  104
cry6Aa    --------------MIIDSKTTLPRHSLIHTIKLNSNKKYGPGDMTN----------GNQFIIS  40
cry7Aa    Q-------PEALASGNTAINTVVSVTGATLSALGVPGASFITN--------FYLKIAGLL  92
cry8Aa    NP-ELFGNPETFIS-SSTIQTGIGIVGRILGALGVPFASQIAS--------FYSFIVGQL  102
cry10Aa   QQYGNNAGNFASSETIVGVSAGIIVVGTMLGAFAAPVLAAG--------IISFGTLLPIF  106
cry16Aa   H-----IENPREASVRAGLGKGLGIVSTIVGFFGGSIILDTIG-------LFYQISELL  101
cry19Ba   S-----YASSGPSQL---FKVGGSIVAKILG-----MIPEVGP-------LLSWMVSLF  93
cry24Aa   N-----------ISPSPAAAITSKIVSIVLKTLAKAVASSLAD---------SIKSSLG  90
                              :        :


axmi007   WPAGEQDKTVWTQFIKMGEIFVDTPLTESIKQLKLQTLEGFRQILQ---SYNTALDDWRK  172
cry1Aa    GPS--Q----WDAFPVQIEQLINQRIEEFARNQAISRLEGLSNLYQ---IYAESFREWEA  119
cry1Ac    GPS--Q----WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQ---IYAESFREWEA  119
cry1Ia    WP---KGKNQWEIFMEHVEEIINQKISTYARNKALTDLKGLGDALA---VYHDSLESWVG  147
cry3Aa1   WPS--E--DPWKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVE---DYVSALSSWQK  160
cry3Ba    WPS--DA-DPWKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE---DYVNALDSWKK  161
cry4Aa    FPAQDQS-NTWSDFITQTKNIIKKEIASTYISNANKILNRSFNVIS---TYHNHLKTWE-  159
cry6Aa    KQE-------WATIGAYIQTGLGLPVNEQQLRTHVNLSQDISIPSDFSQLYDVYCS----  89
cry7Aa    WPE--NGKI-WDEFMTEVEALIDQKIEEYVRNKAIAELDGLGSALD---KYQKALADWLG  146
cry8Aa    WPS--KSVDIWGEIMERVEELVDQKIEKYVKDKALAELKGLGNALD---VYQQSLEDWLE  157
cry10Aa   WQGSDPA-NVWQDLLNIGGRPIQ-EIDKNIINVLTSIVTPIKNQLD---KYQEFFDKWEP  161
cry16Aa   WPEDDTQQYTWQDIMNHVEDLIDKRITEVIRGNAIRTLADLQGKVD---DYNNWLKKWKD  158
cry19Ba   WPTIEEKNTVWEDMIKYVANLLKQELTNDTLNRATSNLSGLNESLN---IYNRALAAWKQ  150
cry24Aa   ISKTITENNVSQVSMVQVHQIINRRIQETILDLGESSLNGLVAIYNR--DYLGALEAWNN  148
                   :      :                              *
```

Fig. 1A

```
axmi007    LKRLQAPGLPPSSALQQAALTLKIRFENVHNDFIREIPG--FQLETYKTLLLPIYAQAAN 230
cry1Aa     -----DPTN---PALREEMRIQFNDMNSALTTAIPLLAVQ-----NYQVPLLSVYVQAAN 166
cry1Ac     -----DPTN---PALREEMRIQFNDMNSALTTAIPLFAVQ-----NYQVPLLSVYVQAAN 166
cry1Ia     -----NRNN---TRARSVVKSQYIALELMFVQKLPSFAVS-----GEEVPLLPIYAQAAN 194
cry3Aa1    -----NPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAIS-----GYEVLFLTTYAQAAN 210
cry3Ba     -----APVNLRSRRSQDRIRELFSQAESHFRNSMPSFAVS-----KFEVLFLPTYAQAAN 211
cry4Aa     ----NNPNPQNTQDVRTQIQLVHYHFQNVIPELVNSCPPNPSDCDYYNILVLSSYAQAAN 215
cry6Aa     --------------DKTSAEWWNKNLYPLIIKSANDIASY-----GFKVAGDPSIKKDG- 129
cry7Aa     -----KQDD---PEAILSVATEFRIIDSLFEFSMPSFKVT-----GYEIPLLTVYAQAAN 193
cry8Aa     -----NRND---ARTRSVVSNQFIALDLNFVSSIPSFAVS-----GHEVLLLAVYAQAVN 204
cry10Aa    ---------ARTHANAKAVHDLFTTLEPIIDKDLDMLKN----NASYRIPTLPAYAQIAT 208
cry16Aa    ----DPKSTGNLSTLVTKFTALDSDFNGAIRTVNNQGSP------GYELLLLPVYAQIAN 208
cry19Ba    ----NKNNFASGELIRSYINDLHILFTRDIQSDFSLG--------GYETVLLPSYASAAN 198
cry24Aa    --------NKSNINYQTNVAEAFKTVEREFFTKLKGIYRTS----SSQITLLPTFTQAAN 196
                                                                .   .   .


axmi007    FHLNLLQQGAELADEWNADIHPSQIEPNAGTSDDYYK-LLKENIPKYSNYCANTYREGLN 289
cry1Aa     LHLSVLRDVSVFGQRWGFDA----------ATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
cry1Ac     LHLSVLRDVSVFGQRWGFDA----------ATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
cry1Ia     LHLLLLRDASIFGKEWGLSS----------SEISTFYNRQVERAGDYSDHCVKWYSTGLN 244
cry3Aa1    THLFLLKDAQIYGEEWGYEK----------EDIAEFYKRQLKLTQEYTDHCVKWYNVGLD 260
cry3Ba     THLLLLKDAQVFGEEWGYSS----------EDIAEFYQRQLKLTQQYTDHCVNWYNVGLN 261
cry4Aa     LHLTVLNQAVKFEAYLKNNRQFDYLEPLP-TAIDYYP-VLTKAIEDYTNYCVTTYKKGLN 273
cry6Aa     -YFKKLQDELDNIVDNNSDD---------------DAIAKAIKDFKARCGILIKEAKQ 171
cry7Aa     LHLALLRDSTLYGDKWGFTQ----------NNIEENYNRQKKRISEYSDHCTKWYNSGLS 243
cry8Aa     LHLLLLRDASIFGEEWGFTP----------GEISRFYNRQVQLTAEYSDYCVKWYKIGLD 254
cry10Aa    WHLNLLKHAATYYNIWLQN---QGINPSTFNSSNYYQGYLKRKIQEYTDYCIQTYNAGLT 265
cry16Aa    LHLLLLRDAQIYGDKWWSAR--------ANARDNYYQIQLEKTKEYTEYCINWYNKGLN 259
cry19Ba    LHLLLLRDVAIYG-KELGYP--------STDVEFYYNEQKYYTEKYSNYCVNTYKSGLE 248
cry24Aa    LHLSMLRDAVMYQEGWNLQS-----------HINYSKELDDALEDYTNYCVEVYTKGLN 244
                ::   *..                                    .:.   .       .


axmi007    KLRNEP------NMRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTELT 343
cry1Aa     RVWGPDS------RDWVRYNQFRRELTLTVLDIVALFSNYDSRRYP------IRTVSQLT 264
cry1Ac     RVWGPDS------RDWVRYNQFRRELTLTVLDIVALFPNYDSRRYP------IRTVSQLT 264
cry1Ia     NLRGTNA------ESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYP------IKTTAQLT 292
cry3Aa1    KLRGSSY------ESWVNFNRYRREMTLTVLDLIALFPLYDVRLYP------KEVKTELT 308
cry3Ba     SLRGSTY------DAWVKFNRFRREMTLTVLDLIVLFPFYDVRLYS------KGVKTELT 309
cry4Aa     LIKTTPDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYP------IGVQSELT 327
cry6Aa     YEEAAKN----IVTSLDQFLHGDQKKLEGVINIQKRLKEVQTALNQA-----HGESSPAH 222
cry7Aa     RLNGSTY------EQWINYNRFRREMILMALDLVAVFPFHDPRRYS------METSTQLT 291
cry8Aa     KLKGTTS------KSWLNYHQFRREMTLLVLDLVALFPNYDTHMYP------IETTAQLT 302
cry10Aa    MIRTNT------NATWNMYNTYRLEMTLTVLDLIAIFPNYDPEKYP------IGVKSELI 313
cry16Aa    DFRTAGQ--------WVNFNRYRREMTLTVLDIISMFPIYDARLYPT------EVKTELT 305
cry19Ba    SKKQIG---------WSDFNRYRREMTLSVLDIVALFPLYDTGLYPSKDGK-IHVKAELT 298
cry24Aa    ALRGSTA------IDWLEFNSFRRDMTLMVLDLVAIFPNYNPVRYP------LSTKISLS 292
                        :         .::        :       :
```

Fig. 1B

```
axmi007   REIYTTEINFDRLTYL-------EIQPNLAIMEYNLTRSGLRLFSFLDELIFYTKNETYG 396
cry1Aa    REIYTNPVLENFDGS---------FRG--MAQRIEQNIRQPHLMDILNSITIYTDVHRGF 313
cry1Ac    REIYTNPVLENFDGS---------FRG--SAQGIERSIRSPHLMDILNSITIYTDAHRGY 313
cry1Ia    REVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLS--R 350
cry3Aa1   RDVLTDPIVGVNNLR---------GYGTTFSNIEN-YIRKPHLFDYLHRIQFHTRFQPGY 358
cry3Ba    RDIFTDPIFTLNALQ---------EYGPTFSSIEN-SIRKPHLFDYLRGIEFHTRLRPGY 359
cry4Aa    REIY-QVLNFEESPYK-------YYD--FQYQEDSLTRR-PHLFTWLDSLNFYEKAQTTP 376
cry6Aa    KELLEKVKNLKTTLER-----------TIKAEQDLEKKVEYSFLLGPLLGFVVYEILEN 270
cry7Aa    REVYTDPVSLSISNP--------DIGPSFSQMENTAIRTPHLVDYLDELYIYTSKYKAF 342
cry8Aa    RDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVIRPPHLFDILSSVEINTSRGGIT 362
cry10Aa   REVY---TNVNSDTFR-------TIT----ELENGLTRN-PTLFTWINQGRFYTRNSRDI 358
cry16Aa   REIYSDVINGEIYGLM-------TPYFSFEKAESLYTRA-PHLFTWLKGFRFVTNSISYW 357
cry19Ba   REIYSDVINDHVYGLM-------VPYISFEHAESLYTRR-PHAFTWLKGFRFVTNSINSW 350
cry24Aa   RKIYTDPVGRTDSPSFG-DWTNTGRTLANFNDLEREVTDSPSLVKWLGDMTIYTGAIDSY 351
                   :.:                               .        :

axmi007   NRLVGIAN-RNRSTYATTGTEIIYGERTGPPTT-KTLIPFESYKVSIVTDRQVTPTSPFP 454
cry1Aa    N--------YWSGHQITASPVGFSGPEFAFPLFGNAGNAAPP-VLVSLTGLGIFRTLSSP 364
cry1Ac    Y--------YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST 365
cry1Ia    WSNTQYMN-MWGGHKLEFRTIGGTLNISTQ----GSTNTSINPVTLPFTSRDVYRTESLA 405
cry3Aa1   YGNDSFN--YWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQ--NLEFNGEKVYRAVANT 414
cry3Ba    SGKDSFN--YWSGNYVETRPSIGSNDTITSPFYGDKSIEPIQ--KLSFDGQKVYRTIANT 415
cry4Aa    NNFFTSHY-NMFHYTLDNISQKSSVFGNHNVTD-KLKSLGLATNIYIFLLNVISLDNKYL 434
cry6Aa    TAVQHIKN--QIDEIKKQLDSAQHDLDRDVKIIGMLNSINTDIDNLYSQGQEAIKVFQKL 328
cry7Aa    SHEIQPDLFYWSAHKVSFKKSEQSN-LYTTGIYGKTSGYISS-GAYSFHGNDIYRTLAAP 400
cry8Aa    LNNDAYIN-YWSGHTLKYRRTADSVTYTA----NYGRITSEKNSFALEDRDIFEINSTV 417
cry10Aa   LDPYDIFS-FTGNQMAFTHTNDDRNIIWGAVHG-NIISQDTSKVFPFYRNKPIDKVEIVR 416
cry16Aa   TFLSGGQN-KYSYTN-NSSINEGSFRGQDTDYGGTSSTINIPSNSYVYNLWTENYEYIYP 415
cry19Ba   TFLSGGEN-RYFLTHGEGTIYNGPFLGQDTEYGGTSSYIDISNNSSIYNLWTKNYEWIYP 409
cry24Aa   RPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNILYDDIYKLDLRA 411


axmi007   N-IYFTINQIELYLNNSP--SNKLTYSAGGNLSNDKKTTDFQFPVKKDCKPII--NPNCL 509
cry1Aa    ---LYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPSTIYRQRGTVDSLDVIPPQDNSV 421
cry1Ac    ---LYRRPFN-IGINNQQLSVLDGTEFAYG-TSSNLPSAVYRKSGTVDSLDEIPPQNNNV 420
cry1Ia    GLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIG--TQLQDSENELPPEATGQ 463
cry3Aa1   NLAVWP-SAVYSGVTKVEFSQYNDQTDEASTQTYDSKRN-VGAV-SWDSIDQLPPETTDE 471
cry3Ba    DIAAFPDGKIYFGVTKVDFSQYDDQKNETSTQTYDSKRY-NGYLGAQDSIDQLPPETTDE 474
cry4Aa    N-DYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGLPILKRRENQG--NPTLF 491
cry6Aa    QGIWATIGAQIENLRTTSLQEVQDSDDADEIQIELEDASDAWLVVAQEARD--------- 379
cry7Aa    SVVVYPYTQN-YGVEQVEFYGVKGHVHYRGDNKYDL--------TYDSIDQLPPDGE-- 448
cry8Aa    ANLANYYQKAYGVPGSWFHMVKRGTSSTTAYLYSKTHTALQGCTQVYESSDEIPLDRT-V 476
cry10Aa   HREYSDIIYEMIFFSNSS---EVFRYSSNSTIENNYKRTDSYMIPKQTWKN--------- 464
cry16Aa   WGDPVNITKMNFSVTDNN--SSKELIYGAHRTNKPVVRTDFDFLTNKEGTE-------L 465
cry19Ba   WTDPVNITKINFSITDNS--NSSESIYGAERMNKPTVRTDFNFLLNRAGNG-------P 459
cry24Aa   AAVSTIQGAMDTTFGVSSSRFFDIRGRNQLYQSNKPYPSLPITITFPGEESSE------ 464
```

Fig. 1C

```
axmi007    PSYNSYSHILSQFSLFNYSYKIGLALNILYTGALGWTHSSVNRNNAISDKIITMIPAIKG  569
cry1Aa     PPRAGFSHRLSHVTMLSQAAG---AVYTLRAPTFSWQHRSAEFNNIIPSSQITQIPLTKS  478
cry1Ac     PPRQGFSHRLSHVSMFRSGFSNS-SVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKG  479
cry1Ia     PNYESYSHRLSHIGLISASHVK--ALVYS------WTHRSADRTNTIEPNSITQIPLVKA  515
cry3Aa1    PLEKGYSHQLNYVMCFLMQGSR------GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKA  525
cry3Ba     PLEKAYSHQLNYAECFLMQDRR------GTIPFFTWTHRSVDFFNTIDAEKITQLPVVKA  528
cry4Aa     PTYDNYSHILSFIKSLSIP-----ATYKTQVYTFAWTHSSVDPKNTIYTHLTTQIPAVKA  546
cry6Aa     ----------------------------FTLNAYSTNSRQNLPINVISDSCNCST       406
cry7Aa     PIHEKYTHRLCHATAIFKSTP---DYDNATIPIFSWTHRSAEYYNRIYPNKITKIPAVKM  505
cry8Aa     PVAESYSHRLSHITSHSFSKNG--SAYYGSFPVFVWTHTSADLNNTIYSDKITQIPAVKG  534
cry10Aa    ---EEYGHTLSYIKTDNYIFS---VVRERRRVAFSWTHTSVDFQNTIDLDNITQIHALKA  518
cry16Aa    AKYNDYNHILSYMLINGETFG-----QKRHGYSFAFTHSSVDPNNTIAANKITQIPVVKA  520
cry19Ba    TTYNDYNHILSYMLINGETFG-----QKRHGYSFAFTHSSVDRYNTIVPDKIVQIPAVKT  514
cry24Aa    GNANDYSHLLCDVKILQEDSSN-ICEGRSSLLSHAWTHASLDRNNTILPDEITQIPAVTA  523
                               *  :    :  :                      .
```

```
axmi007    NSLDTNSKVIEGPGHTGGNLVYLQSQGR-------LEITCRTPNSTQSYYIRLRYATNGA  622
cry1Aa     TNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYASTTN  533
cry1Ac     NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP  538
cry1Ia     FNLSSGAAVVRGPGFTGGDILRRTNGTFGDIRVNINPPF-----AQRYRVRIRYASTTD  570
cry3Aa1    YKLQSGASVVAGPRFTGGDIIQCTENG----SAATIYVTP-DVSYSQKYRARIHYASTSQ  580
cry3Ba     YALSSGASIIEGPGFTGGNLLFLKESSN---SIAKFKVTLNSAALLQRYRVRIRYASTTN  585
cry4Aa     NSLGTASKVVQGPGHTGGDLIDFKDH---------FKITCQHSNFQQSYFIRIRYASNGS  597
cry6Aa     TNMTSNQYSNPTTNMTS---------------------------NQYMISHEYTSLPN    437
cry7Aa     YKLDDPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNSPL-----SQKYRVRVRYATNVS  560
cry8Aa     DMLYLGGSVVQGPGFTGGDILKRTNPSILGTFAVTVNGSL-----SQRYRVRIRYASTTD  589
cry10Aa    LKVSSDSKIVKGPGHTGGDLVILKDSMD-------FRVRFLKN-VSRQYQVRIRYATNAP  570
cry16Aa    SSINGSISIEKGPGFTGGDLVKMRADSG-------LTMRFKAELLDKKYRVIRYKCNYS  573
cry19Ba    NLVG--ANIIKGPGHTGGDLLKLEYERF------LSLRIK-LIASMTFRIRIRYASNIS  564
cry24Aa    YELRGNSSVVAGPGSTGGDLVKMSYHS--------VWSFKVYCSELKNYRVRIRYASHGN  575
                :        .  *.                               :     .*
```

```
axmi007    GNTLPNISLTIPGVIGIPPQRLNNTFSGTNYNNLQYGDFGYFQFPSTVTLPLNR--NIPF  680
cry1Aa     LQFHTSIDGRPINQGNFS-------ATMSSGSNLQSGSFRTVGFTTPFNFSNGS---SVF  583
cry1Ac     IHLNVNWGNSSIFSNTVP-------ATATSLDNLQSSDFGYFESANAFTSSLGN------  585
cry1Ia     LQFHTSINGKAINQGNFS-------ATMNRGEDLDYKTFRTVGFTTPFSFLDVQ---STF  620
cry3Aa1    ITFTLSLDGAPFNQYYFD-------KTINKGDTLTYNSFNLASFSTPFELSG-----NNL  628
cry3Ba     LRLFVQNSNNDFLVIYIN-------KTMNIDGDLTYQTFDFATSNSNMGFSGDT---NDF  635
cry4Aa     ANTRAVINLSIPGVAELG-MALNPTFSGTDYTNLKYKDFQYLEFSNEVKFAPNQ--NISL  654
cry6Aa     NFMLSRNSNLEYKCPENN-----------FMIYWYNNSDWYNNSDWYNN----------  475
cry7Aa     GQFNVYINDKITLQTKFQN----TVETIGEGKDLTYGSFGYIEYSTTIQFPDEH---PKI  613
cry8Aa     FEFTLYLG-DTIEKNRFN-------KTMDNGASLTYETFKFASFITDFQFRETQ---DKI  638
cry10Aa    KTTVFLTGIDTISVELPS----TTSRQNPNATDLTYADFGYVTFPRTVPNKTFEGEDTLL  626
cry16Aa    SKLILRKWKGEGYIQQQI------HNISPTYGAFSYLESFTITTTENIFDLTME-VTYPY  626
cry19Ba    GQMMINIGYQNPTYFNII------PTTSRDYTELK-FEDFQLVDTSYIYSGGPS-ISS--  614
cry24Aa    CQFLMKRWPSTGVAPRQWAR---HNVQGTFSNSMRYEAFKYLDIFTITPEENNF------  626
```

Fig. 1D

```
axmi007   IFNRADVSN-SILIIDKIEFIPITSSVRQNREKQKLETIQTKINTFFTNHTKNTLNIEAT 739
cry1Aa    TLSAHVFNSGNEVYIDRIEFVPAEVTFEA---EYDLERAQKAVNELFTSSNQIGLKTDVT 640
cry1Ac    IVGVRNFSGTAGVIIDRFEFIPVTATLEA---EYNLERAQKAVNALFTSTNQLGLKTNVT 642
cry1Ia    TIGAWNFSSGNEVYIDRIEFVPVEVTYEA---EYDFEKAQEKVTALFTSTNPRGLKTDVK 677
cry3Aa1   QIGVTGLSAGDKVYIDKIEFIPVN--------------------------------- 652
cry3Ba    IIGAESFVSNEKIYIDKIEFIPVQ--------------------------------- 659
cry4Aa    VFNRSDVYTNTTVLIDKIEFLPITRSIREDREKQKLETVQQIINTFYANPIKNTLQSELT 714
cry6Aa    --------------------------------------------------------
cry7Aa    TLHLSDLSNNSSFYVDSIEFIPVDVNYAE---KEKLEKAQKAVNTLFTE-GRNALQKDVT 669
cry8Aa    LLSMGDFSSGQEVYIDRIEFIPVDETYEA---EQDLEAAKKAVNALFTNTKD-GLRPGVT 694
cry10Aa   MTLYGTPNHSYNIYIDKIEFIPITQSVLDYTEKQNIEKTQKIVNDLFVN---------- 675
cry16Aa   GRQFVEDIPS--LILDKIEFLPTN------------------------------- 648
cry19Ba   NTLWLDNFSNGPVIIDKIEFIPLGITLNQAQGYDTYDQNANGMYHQNYSNSGYNYNQEYN 674
cry24Aa   -AFTIDLESGGDLFIDKIEFIPVSGSAFEYEGKQNIEKTQKAVNDLFIN---------- 674


axmi007   NYDID--------------------------------------------------- 744
cry1Aa    DYHIDQVSNLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWR 700
cry1Ac    DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG 702
cry1Ia    DYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM---------------- 719
cry3Aa1   --------------------------------------------------------
cry3Ba    --------------------------------------------------------
cry4Aa    DYDIDQAANLVECISEELYPKEKMLLLDEVKNAKQLSQSRNVLQNGDFE----SATLGWT 770
cry6Aa    --------------------------------------------------------
cry7Aa    DYKVDQVSILVDCISGDLYPNEKRELQNLVKYAKRLSYSRNLLLDPTFDSINSSEENGWY 729
cry8Aa    DYEVNQAANLVECLSDDLYPNEKRLLFDAVREAKRLSGARNLLQDPDFQEING--ENGWA 752
cry10Aa   --------------------------------------------------------
cry16Aa   --------------------------------------------------------
cry19Ba   TYYQSYNN----------------------------------------------- 682
cry24Aa   --------------------------------------------------------
```

Fig. 1E